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Genetic variability of Ginger (*Zingiber officinale* Rosc.) Collections for Growth and Yield Characters

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ABSTRACT: Ginger is grown as a number of landraces and locally popular cultivars in Karnataka, India and there is a need for the assessment of variability present among landraces and locally popular cultivars growing in Karnataka. Therefore, a set of 45 ginger collections were collected from several parts of Karnataka was subjected to field evaluation in augmented block design by using four checks in four blocks. This investigation was conducted to study the genetic variability of ginger collections for growth and yield parameters. For all of the parameters studied, there was a broad genetic variation among the collections; high PCV and GCV was recorded in dry rhizome yield per hectare, followed by rhizome yield per hectare, length of the primary rhizome, rhizome yield per plant and number of secondary rhizome, respectively. In every case, high phenotypic variances were observed than the genotypic variances. Depends on high heritability together with high genetic advance as per cent of mean, number of secondary rhizomes, length of the primary rhizome, rhizome yield per plant, length of secondary rhizome, girth of secondary rhizome, girth of primary rhizome and number of primary rhizomes were identified as superior traits and exhibit additive genetic variance. These characteristics would be considered in effective selection.

Keywords: Genetic variability, PCV, GCV, heritability, genetic advance.

INTRODUCTION

Ginger (*Zingiber officinale* Rosc.) is one of the ancient oriental spice and is being grown in tropical and subtropical area (Yonzone *et al*., 2021) for its rhizomes which is used both as dried spice and as a fresh vegetable, since time immemorial. Ginger comes under the family Zingiberaceae and commonly used as a spice, in pickles, candies, and as a medicine to treat gastrointestinal disorders such dyspepsia, nausea and diarrhea (Karthik *et al.*, 2017a). Ginger anti-inflammatory and anti-nausea properties are used in the pharmaceutical sector. Ginger is used in traditional health products because it works well as an appetite stimulant, a cold preventative and a strong antioxidant (Verma and Bisen 2022). It has been therapeutically used in many Ayurvedic formulations from the ancient period and is also known as "Maha Aushadhi- A Great Medicine" (Abdulwase *et al*., 2020). World ginger production is estimated to be 4.90 million tonnes with an area of 0.45 million hectares and it is mainly distributed in India, Indonesia, China, Nigeria, Thailand, Bangladesh, Philippines, Nepal and Jamaica. India is the largest producer of ginger contributing to about 45.31 per cent, followed by China, Nepal, Nigeria, Thailand and Bangladesh (Anonymous, 2021). The average productivity of the crop at present in India is low (11.31 tonnes per ha). There is a tremendous opportunity to increase the productivity and there by the total production. As ginger is propagated through vegetative means, flowers are seldom formed and no seed setting takes place. Conventional breeding methods like hybridization is not possible because of this nature of the crop therefore, selection is the easiest method of improving the crop as compare to mutation and polyploidy breeding (Babu *et al*., 2013).

In India, the available germplasm is the most valuable natural source of donor parents to improve specific plant traits through genetic reconstruction (Hawkes, 1981). Germplasm conservation is an important

technique for conservation of the plant diversity for any of the country (Shivakumar, 2019). As a result, germplasm collection, conservation, and evaluation are important for present and future crop improvement programmes. This variability can be utilized to improve the crop through selection (Anargha *et al*., 2020). Propagated through vegetative means, the crop could accumulate mutants over a period of time would have rendered the collection to be a mixture of germplasm. Though the crop is cultivated since decades farmers do not know the exact name of cultivar, they were telling that these are local cultivars, the seed rhizome materials are collected from relatives or maintained by forefathers are being used for cultivation, hence, it is essential to collect all genotypes/landraces, prevailing in the region of Karnataka. The purpose of this investigation was to ascertain the extent of genetic variability in ginger collections from different parts of Karnataka through the study of variance components, heritability and genetic advance to select superior genotypes for future crop improvement.

MATERIAL AND METHODS

A. Study site and plant material

The experimental field was located at an altitude of 619 m above MSL 14° 37'10"North latitude and 70°50' East-longitude in the *Western Ghats* (Zone 9 of region-2) of Karnataka, the research field of Plantation, Spices, Medicinal and Aromatic Crops Department, College of Horticulture, Sirsi, Karnataka, India during 2020-21. Experimental site soil was red lateritic in nature with a p^H of 5.5. Ginger samples from major taluks of Hassan, Shivamogga, Mysore, Bidar, Chikmagaluru, Kodagu, Haveri, Uttar Kannada, Mandya, Kalburgi and Belgaum districts were collected from farmer fields were termed as collections. Major *taluks* and villages where ginger is intensively cultivated were covered for the sampling. The sampling strategy ensured to represent maximum genetic diversity. At each sampling location 2-3 eye buds per rhizome to account for about 30 numbers were collected. A set of 45 ginger collections from Karnataka along with the four improved varieties as checks, was subjected to field evaluation. The ginger accessions used in the study are presented in Table 1.

B. Experimental design and agronomic practices

The main field was prepared to fine tilth by ploughing and harrowing and the FYM @ 25 t/ha was incorporated into the soil. The field evaluation of all the accessions was done in an Augmented Block Design with four checks IISR-Mahima, IISR-Varada, Rio-de-Jeneiro and Humnabad Local respectively in four blocks. Each accession was sown in the raised bed by using two seed rhizome units from each rhizome by following collection to row planting, about 24 plants per plot/bed. Efforts were made by selecting uniform seed rhizomes to ensure least influence on the phenotype. A spacing of 45 × 30 cm in raised beds of 2.5 × 1.3 m size was followed. The land was fertilized with 100, 50 and 50 kg of N, P and K ha^{-1}, respectively. UHS, Bagalkot (Anonymous, 2022) package of practices were followed to perform all agronomic practices. Observations on growth and yield parameters were recorded.

C. Collection of data and analysis

The data was recorded on different parameters from all the plants of each treatment, mean data was used for statistical analysis for eighteen diverse traits *viz.*, plant height (cm), number of shoots per plant, height of shoot (cm), number of leaves on main shoot, leaf petiole length (cm), leaf area per plant (cm^2), leaf area index, number of primary rhizomes, length of primary rhizome (cm), girth of primary rhizome (cm), number of secondary rhizome, length of secondary rhizome (cm), girth of secondary rhizome (cm), rhizome yield per plant (g), rhizome yield per hectare (t), dry rhizome yield (t/ha), recovery percentage (%) and crop duration. The analysis of variance (ANOVA) for augmented block design was estimated according to Fischer's method of analysis of variance given by Federer and Raghavrao (1975) for analysis and interpretation of data. According to Burton and Devane (1953) genotypic and phenotypic coefficient of variability was calculated. Broad sense heritability was calculated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956). According to the formula given by Johnson *et al.* (1955) genetic advance (GA) was computed.

RESULTS AND DISSCUSSION

The analysis of variance for growth and yield parameters in ginger indicated a significantly higher amount of variability present among the collections for all the 18 characters studied (Table 2 and 3). Most of the characters studied shows significant variation except number of shoots per plants, height of the shoot and number of leaves on main shoot. The ginger population's significant variation for all attributes under study suggested that the high degree of genetic variability present among the ginger collection in Karnataka, India. This is consistent with studies by Aragaw *et al*. (2011), which found substantial genetic variation in ginger that was collected from Ethiopia. (Ravishanker *et al*., 2013) revealed similar findings regarding variability for agronomic characteristics of ginger such as plant height, tiller thickness, rhizome thickness, and days taken to harvest.

The phenotypic coefficients of variability (PCV) were found high for dry rhizome yield per hectare (39.55%), rhizome yield per hectare (38.23%), length of the primary rhizome (32.89%), rhizome yield per plant (27.83%), number of secondary rhizomes (27.54%), girth of the primary rhizome (25.93%), girth of the secondary rhizome (25.83%), number of primary rhizomes (25.14%), length of secondary rhizome (24.89%), leaf area (23.15%) and leaf area index (23.15%) respectively. In contradictory to present studies, Dev and Sharma (2022) found high PCV for yield $plant^{-1}$ $plot^{-1}$ ha^{-1}, weight of mother, primary and secondary rhizomes, number of secondary rhizomes $plant^{-1}$ and number of tillers $plant^{-1}$. This illustrates genetic variability exists among the genotypes in these

characters for making further improvement through clonal selection. Similar results for different characters were reported to various extents by Medhi *et al*. (2007); Islam *et al*. (2008); Blanco and Pinheiro (2017) and Dev and Sharma (2022b) in turmeric.

High GCV was found for dry rhizome yield per hectare, rhizome yield per hectare, length of the primary rhizome, rhizome yield per plant and number of secondary rhizomes. For all the characters under study, PCV estimates were generally higher than GCV estimates (Table 4). The GCV was found highest for dry rhizome yield per hectare (37.87%), rhizome yield per hectare (36.75%), length of the primary rhizome (32.88%), rhizome yield per plant (27.81%), number of secondary rhizomes (27.53%), girth of the primary rhizome (25.87%), girth of the secondary rhizome (25.79 %), number of primary rhizomes (25.04%), length of secondary rhizome (24.85%), leaf area (21.6%) and leaf area index (21.6%) respectively. It suggests that the maximum amount of genetic diversity was present, emphasizing the broad range of selection available for enhancing these traits (Ravishanker *et al*., 2013). When the variation between GCV and PCV was minimum for all the characters under study, the environment was predicted to have the least amount of influence (Tiwari, 2003). Nandkangre *et al.* (2016) reported that high GCV was observed for rhizome yield per plant and length of the rhizome. Karthik *et al*. (2017b) also reported high variation for fresh yield plant^{-1}, projected yield hectare^{-1} and yield plot^{-1}respectively. Kalpesh *et al*. (2022) found similar results in mango ginger. The differences in degree of variability may be due to different experimental materials evaluated under various environmental conditions (Dev and Sharma 2022a).

The range of the estimated broad-sense heritability was 99.96 to 55.38%. Heritability estimates were categorized by Dabholkar (1992) as low (5-10%), medium (10-30%), and high (> 30%). For all character under investigation, the broad-sense heritability estimate was high (>50%) based on this scale. Maximum heritability was observed for number of secondary rhizome (99.96%), length of the primary rhizome (99.95%), rhizome yield per plant (99.87%), length of the secondary rhizome (99.74%) and girth of the secondary rhizome (99.68 %) (Table 4). The results of present studies are in line with those reported by Medhi *et al*. (2007) and Islam *et al*. (2008). According to Jalata *et al*. (2011), traits with high heritability values may indicate the existence of more additive gene effects for potential improvement. It has long been known that heritability estimates are helpful in determining the relative importance of selection depends on the phenotypic expression of various traits (Hosseini *et al*., 2012).

The study effect of selection was more accurately predicted by heritability values combined with estimations of genetic advance than by heritability alone (Johnson *et al*., 1955). Rhizome yield per plant, length of the secondary rhizome, girth of the secondary rhizome, number of secondary rhizomes, and primary rhizome length were found to have high heritability estimates related with high genetic advance. Improvement in ginger yield may be achieved through phenotypic selection on the basis of these characteristics. The presence of additive gene action was indicated by high heritability followed by high genetic advance (Abraham and Latha 2003; Jalata *et al*., 2011). The results are in line with Islam *et al*. (2008); Anargha *et al*. (2020) they also reported high heritability together with moderate to high genetic gain for yield and rhizome characters. However, high heritability and genetic gain has been reported by Islam *et al*. (2008) for number of secondary rhizomes, tillers plant^{-1}, plant height and number of primary rhizomes plant^{-1}; Dev and Sharma (2022) for weight of mother, primary and secondary rhizomes. Therefore, selection based on number of secondary rhizome, length of the primary rhizome, rhizome yield per plant, length of the secondary rhizome and girth of the secondary rhizome will be rewarding for increasing of rhizome yield.

Table 1: List of ginger collections from Karnataka used in the study.

Sr. No.	Name of collections	Location	District	Sr. No.	Name of collections	Location	District
1.	FBG-CTP	Chitgoppa	Bidar	24.	FBG-ARK-2	Arkalgudu	Hassan
2.	FBG-HBD	Humnabad	Bidar	25.	FBG-ALR-1	Alur	Hassan
3.	FBG-BDR-1	Bidar	Bidar	26.	FBG-ALR-2	Alur	Hassan
4.	FBG-BDR-2	Bidar	Bidar	27.	FBG-HNP	Holenarasipura	Hassan
5.	FBG-JWG	Jewargi	Kalburgi	28.	FBG-KRP-1	Krishnarajpete	Mandya
6.	FBG-SMG-1	Shivamogga	Shivamogga	29.	FBG-KRP-2	Krishnarajpete	Mandya
7.	FBG-SMG-2	Shivamogga	Shivamogga	30.	FBG-MVL	Malavalli	Mandya
8.	FBG-SKR-1	Shikaripur	Shivamogga	31.	FBG-NML-1	Nagamangala	Mandya
9.	FBG-SKR-2	Shikaripur	Shivamogga	32.	FBG-NML-2	Nagamangala	Mandya
10.	FBG-SRB-1	Soraba	Shivamogga	33.	FBG-CKM-1	Chickmagalur	Chickmagalur
11.	FBG-SRB-2	Soraba	Shivamogga	34.	FBG-CKM-2	Chickmagalur	Chickmagalur
12.	FBG-THL	Thirthahalli	Shivamogga	35.	FBG-MDG-1	Mudigere	Chickmagalur
13.	FBG-RTL-1	Rattihalli	Haveri	36.	FBG-MDG-2	Mudigere	Chickmagalur
14.	FBG-RTL-2	Rattihalli	Haveri	37.	FBG-HSR	Hunsur	Mysore
15.	FBG-HKR-1	Hirekerur	Haveri	38.	FBG-HDK-1	HD Kote	Mysore
16.	FBG-HKR-2	Hirekerur	Haveri	39.	FBG-HDK-2	HD Kote	Mysore
17.	FBG-RNR-1	Ranebennur	Haveri	40.	FBG-SWP-1	Somwarpet	Kodagu
18.	FBG-RNR-2	Ranebennur	Haveri	41.	FBG-SWP-2	Somawarpet	Kodagu
19.	FBG-SRS-1	Sirsi	Uttarkannada	42.	FBG-VJP-1	Virajpet	Kodagu
20.	FBG-SRS-2	Sirsi	Uttarkannada	43.	FBG-VJP-2	Virajpet	Kodagu
21.	FBG-SRS-3	Sirsi	Uttarkannada	44.	FBG-KNR	Khanapur	Belgaum
22.	FBG-MGD-1	Mundgod	Uttarkannada	45.	FBG-CKD	Chikkodi	Belgaum
23.	FBG-ARK-1	Arkalgudu	Hassan				

Table 2: Analysis of variance (ANOVA) for growth characters in ginger collections field evaluated during 2020-21.

Source of variation	DF	Mean Sum of Squares						
		PH	NSP	HS	NLMS	LPL	LA	LAI
Blocks	3	1.48	0.12	0.12	0.2	0.001	64137.35	0.04
Entries	48	49.97 **	1.53 **	1.53 **	2.14 **	0.0022 **	1405181.31 **	0.77 **
Checks	3	161.23 **	11.32 **	11.32 **	11.91 **	0.00038 ns	4462957.41 **	2.45 **
Collections	44	43.5 **	0.39	0.39	0.82	0.0012 *	1069614.36 **	0.59 **
Checks vs. Collections	1	0.8	22.43 **	22.43 **	30.91 **	0.05 **	6996798.83 **	3.84 **
Error	9	4.79	0.17	0.17	0.35	0.00038	138719.47	0.08

*Significant at 5 per cent probability level **Significant at 1 per cent probability level

PH: Plant height (cm); NSP: Number of shoots per plant; HS: Height of shoot (cm); NLMS: Number of leaves on main shoot; LPL: Leaf petiole length (cm); LA: Leaf area (cm^2); LAI: Leaf area index

Table 3: Analysis of variance (ANOVA) for yield components of ginger collections field evaluated during 2020-21.

Source of variation	DF	Mean Sum of Squares										
		NPR	LPR	GPR	NSR	LSR	GSR	RYP	RYH	DYH	DR	CD
Blocks	3	0.16 **	0.0016 *	0.03	0.52 **	0.01 **	0.12 **	144.62 **	2.19	0.06	1.55 *	5.76
Entries	48	1.19 **	0.74 **	3.89 **	4.43 **	0.62 **	2.99 **	6092.05 **	9.04 **	0.35 **	8.75 **	105.75 **
Checks	3	1.11 **	0.63 **	1.29 **	5.75 **	0.46 **	2.03 **	8620.22 **	5.72 **	0.28 **	49.36 **	639.48 **
Collections	44	0.66 **	0.76 **	2.7 **	3.78 **	0.64 **	1.96 **	5694.97 **	8.33 **	0.32 **	6.11 **	21.14 **
Checks vs. Collections	1	24.77 **	0.02 **	64.16 **	29.06 **	0.12 **	51.52 **	15979.08 **	50.03 **	1.58 **	2.74 *	2227.34 **
Error	9	0.01	0.00037	0.01	0.0017	0.0016	0.01	7.2	0.63	0.03	0.28	3.11

*Significant at 5 per cent probability level **Significant at 1 per cent probability level

NPR: Number of primary rhizomes LPR: Length of primary rhizome (cm) GPR: Girth of primary rhizome (cm) NSR: Number of secondary rhizomes
LSR: Length of secondary rhizome (cm) GSR: Girth of secondary rhizome (cm) RYP: Rhizome yield per plant (g) RYH: Rhizome yield per hectare (t)
DYH: Dry yield per hectare (t) DR: Dry recovery (%) CD: Crop duration (number of days)

Table 4: Genetic variability parameters for growth and yield characters in ginger collections field evaluated during 2020- 2021.

Trait	Range		Grand mean	PCV (%)	GCV (%)	Heritability (%)	GAM (%)
	Minimum	Maximum					
PH	36.09	62.01	49.93	13.21	12.46	88.99	24.25
NSP	9.50	12.29	10.87	5.66	4.21	55.38	6.47
HS	27.03	47.86	35.58	13.84	13.17	90.66	25.88
NLMS	18.26	21.17	19.99	4.51	3.44	58.11	5.41
LPL	0.53	0.70	0.61	5.59	4.61	68	7.84
LA	2496.13	6483.58	4404.12	23.15	21.6	87.03	41.57
LAI	1.85	4.80	3.26	23.15	21.6	87.03	41.57
NPR	2.15	5.27	3.11	25.14	25.04	99.18	51.45
LPR	1.63	5.70	2.66	32.89	32.88	99.95	67.83
GPR	3.74	9.86	6.14	25.93	25.87	99.55	53.26
NSR	2.90	13.23	6.79	27.54	27.53	99.96	56.78
LSR	1.78	4.98	3.22	24.89	24.85	99.74	51.21
GSR	3.23	8.10	5.24	25.83	25.79	99.68	53.12
RYP	169.91	490.12	268.16	27.83	27.81	99.87	57.34
RYH	8.28	23.52	12.91	38.23	36.75	92.41	72.88
DYH	1.43	4.73	2.44	39.55	37.87	91.65	74.79
DR	14.78	24.13	18.96	13.01	12.71	95.48	25.62
CD	217.24	233.35	226.40	2.04	1.88	85.27	3.59

PH: Plant height (cm) NSP: Number of shoots per plant HS: Height of shoot (cm)
NLMS: Number of leaves on main shoot LPL: Leaf petiole length (cm) LA: Leaf area (cm^2)
LAI: Leaf area index NPR: Number of primary rhizomes LSR: Length of secondary rhizome (cm)
GPR: Girth of secondary rhizome (cm) NSR: Number of secondary rhizomes LSR: Length of secondary rhizome (cm)
GSR: Girth of secondary rhizome (cm) RYP: Rhizome yield per plant (g) RYH: Rhizome yield per hectare (t)
DYH: Dry yield per hectare (t) DR: Dry recovery (%) CD: Crop duration (number of days)

It is recognized that continuous selection for quality and yield variables fixes genetic diversity in crop plants (Desclaux, 2005). The results of this investigation showed that the ginger collections in Karnataka, India, have a wide genetic background. This result is consistent with that of Jatoi *et al*. (2006), who noted a high level of genetic variation in Asian ginger collections.

CONCLUSIONS

The growth and yield characters evaluated had genotypic and phenotypic coefficient of variation in the present study. That demonstrates the genetic diversity of ginger grown in Karnataka, India. The number of secondary rhizomes, length of the primary rhizome, rhizome yield per plant, length of the secondary rhizome and girth of the secondary rhizome were

estimated to have high heritability together with high genetic gain, indicated that clonal selection for these parameters can be successful in ginger.

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Conflict of Interest. None.

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