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Variability studies in ginger

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Abstract
Ginger (*Zingiber officinale* Rosc.) is a very important spice cum medicinal plant having a somatic chromosome number of 2n=22. Ginger has a narrow genetic base and breeding is limited mostly to clonal selection. Polyploidy breeding is one of the frequently used methods in vegetatively propagated horticultural crops to create variability. Colchicine, which is the most widely used chemical for the induction of polyploidy can be applied on the seeds, seedlings, apical shoots, inflorescence, sprouting buds etc. Colchicine can be applied both *in vitro* and *in vivo* to induce polyploids. The most discernable effect of polyploidy has been the increase in yield, essential oil content, production of fertile bridge hybrids and tolerance to biotic and abiotic stresses. Polyploids have greater genetic and biochemical diversity enabling greater ecological tolerance and are expected to have larger geographical ranges than diploids. To comprehend the degree to which the observed variation was due to genetic factors, the value of phenotypic variation, genotypic variation, Environmental variation, co-efficient of variation, phenotypic and genotypic coefficients of variation was obtained.

Keywords: Colchicine, ginger, polyploidy, variability

1. Introduction
India is a leading producer of ginger in the world. Ginger is cultivated in most of the states like Assam, West Bengal, Gujarat, Meghalaya, Mizoram, Karnataka, Andhra Pradesh, Sikkim, Orissa and Kerala, contributing a major share in the country's total production. The major crop improvement objectives in ginger are high yield, bold rhizomes, low fiber, resistance to diseases and improvement in essential oil content and oleoresin. Ginger breeding is limited mostly to clonal selection. This is because ginger displays high sterility [1] as a result of chromosomal aberrations such as translocations and inversions [2, 14, 15] and is propagated by vegetative method creating less variability. Hence other breeding methods such as polyploidy breeding are exploited to create variability.

Polyploidy is generally defined as the possession of three or more complete copies of the nuclear chromosome set. Polyploidy is common in nature and acts as a major mechanism for adaptation and speciation. Approximately 50-70 percent of angiosperms have undergone polyploidy during their evolutionary process [5]. Flowering plants form polyploids at a significant frequency of 1 in every 100,000 plants [6]. Polyploids exhibit increased vigor and also outperform their diploid relatives. The advantages of polyploidy include an increment in plant organs and secondary metabolite content, buffering of deleterious genes and increased heterozygosity.

Natural polyploidy has played an important role in the evolution of spices like black pepper, small cardamom, turmeric, vanilla, saffron etc. All the species of black pepper studied from South India and Sri Lanka could be traced to common basic number 13 while the North Indian species seems to have a basic number of x=12 [17]. The *Mysore* and *Malabar* varieties of cardamom possess 2*n* = 50 and 2*n* = 48 chromosomes, respectively, and aneuploidy as well as structural alterations in the chromosome have contributed to the varietal differentiation [4]. Turmeric is a triploid, hybrid between tetraploid *C. aromatica* and an ancestral diploid *C. longa* (2n=42) type. Intra individual variation occurs in *Vanilla planifolia* with values ranging from 2n=13 to 2n=32 in differentiated cells. This as suggested by [12] might be due to the tight 'side by side' and 'end to end' somatic associations at mitosis that prevent accurate counting of chromosomes at metaphase stage in root tips of *V. planifolia.* This indicates that polyploidization might be an important evolutionary mechanism in vanilla [3].

Developing polyploid individuals artificially would be a remarkable approach to increase vigor. Polyploids mostly exhibit morphological features that are different in forms than their diploid progenies. Polyploidization can be induced by quite a few antimitotic agents.

The most frequently used antimitotic chemicals are colchicine, trifluralin, and Oryzalin. The whole method of induced chromosome doubling consists of a series of steps, including an induction phase, regrowth phase, and a confirmation technique to evaluate the rate of achievement. The induction phase depends on different factors, such as explant types, antimitotic agents, its different concentrations, and exposure durations. To evaluate the accomplishment of polyploidization, morphological or anatomical observations are recorded as a rapid method. However, chromosome count and flow cytometry are the most eminent method for absolute confirmation.

2. Materials and Methods

The experiments conducted at Department of Plantation Crops and Spices, College of Agriculture, Vellayani during 2018 identified four promising genotypes of ginger for yield. Athira and Aswathy are two high yielding varieties of ginger released by KAU from Maran and Rio de Janeiro with an average yield of 21 and 23 t/ha respectively. IISR Varada and IISR Mahima are also high yielding varieties of ginger yielding 22.66 and 23.2 t/ha respectively. An experiment was formulated to produce heteroploids *in vivo* from Athira, Aswathy, Varada, Mahima and the promising four ginger genotypes evaluated in the Department of Plantation Crops and Spices. Thus, a total of eight genotypes and their respective control plants were evaluated. Hundred rhizome bits of each treatment was used in the experiment and single plant observations were undertaken in two generations. The morphological, physiological, cytological, floral and yield observations were carried out in both generations and the genetic analysis was carried out.

2.1 Genetic analysis

2.1.1 Analysis of variance

Per replication mean value of each treatment was used for analysis of variance [13].

Table 1: Sources of variation

Sources of variation	Degree of freedom	Sum of squares	Mean squares	F ratio
Replications	t-1	SSR	MSR	MSR/MSE
Treatment	r-1	SST	MST	MST/MSE
Error	(t-1) (r-1)	SSE	MSE	
Total	rt-1			

Where r = number of replications
t = number of treatments
SSR = sum of squares for replication
SST = sum of squares for treatments
SSE = sum of squares for error

$$\text{Critical Difference, CD} = t_{\alpha}\sqrt{\frac{2MSE}{r}}$$

Where t_{α} indicates students' t table value distribution at error degrees of freedom with level of significance α (5% or 1%).

2.1.2 Estimation of Genetic Parameters

a. Genetic components of variance

The phenotypic and genotypic variances were calculated using the respective mean square values [9].

1. Genotypic variance, $V_G = \frac{MST - MSE}{r}$
2. Environmental variance, $V_E = MSE$
3. Phenotypic variance, $V_P = V_G + V_E$

b. Coefficient of variation

Genotypic, Phenotypic and Environmental Coefficient of Variation were estimated from V_P, V_G and V_E, expressed in percentage for each trait.

1. Genotypic coefficient of variation, GCV = $\frac{\sqrt{VG}}{X} \times 100$
2. Phenotypic coefficient of variation, PCV = $\frac{\sqrt{VP}}{X} \times 100$
3. Environmental coefficient of variation, GCV = $\frac{\sqrt{VE}}{X} \times 100$

Where,
X= Grand mean
[18] Reported following categories for the range of variation.
High: >20 percent
Medium: 10-20 percent
Low: <10 percent

3. Results

Genotypic variance was highest for fresh rhizome yield plant^{-1} (1246.20) followed by pollen fertility percentage (281.95). Genotypic variance for number of leaves per plant, plant height, and dry rhizome yield per plant was 239.79, 59.08 and 47.09 respectively. Phenotypic variance was found to be the highest for fresh rhizome yield plant^{-1} (3595.27) which was followed by pollen fertility percentage (323.31). Phenotypic variance for number of leaves per plant, dry rhizome yield per plant and plant height was 260.20, 90.88 and 72.85 respectively. Environmental variance was found to be the highest for fresh rhizome yield (2349.07) which was followed by dry rhizome yield per plant (43.79). Environmental variation for pollen fertility percentage, dry matter production and number of leaves per plant was 41.36, 27.16 and 20.41 respectively (Table 2). The value of coefficient of variation (CV) ranged from 2.48 percent for oleoresin to 32.32 percent for photosynthetic rate. The characters like fresh rhizome yield per plant (19.78%) and stomatal conductance (18.93%) showed high value of coefficient of variation. Moderate coefficient of variation was observed for dry rhizome yield per plant (13.85%), number of tillers per plant (12.53%), harvest index (11.15%) and pollen fertility percentage (10.99%). The characters like essential oil content (7.96%), leaf area index (6.82%), dry matter production (5.54%), plant height (5.32%), number of leaves per plant (5.24%) and leaf area (4.42%) recorded lowest values of coefficient of variation.

The value of phenotypic coefficient of variation (PCV) ranged from 7.88 percent for oleoresin content to 43.40 percent for stomatal conductance. The characters like photosynthetic rate (42.00%), pollen fertility percentage (30.74%), leaf area index (26.58%) and fresh rhizome yield per plant (24.48%) showed high value of phenotypic coefficient of variation. Moderate phenotypic coefficient of variation was observed in dry rhizome yield per plant (19.95%), number of leaves per plant (18.69%), number of tillers per plant (15.46%), Harvest index (14.40%) and plant height (12.23%). The characters like

essential oil content (10.94%), leaf area (10.16%) and dry matter production (8.34%) recorded lowest values of phenotypic coefficient of variation. The estimates of PCV were higher than GCV for all the traits studied which is an indicator of the additive effect of the environment on the expression of the trait. The genotypic coefficient of variation (GCV) ranged from 6.24 percent for dry matter production to 39.06 percent for stomatal conductance. High GCV was observed for pollen fertility percentage (28.71%), photosynthetic rate (26.83%) and leaf area index (25.68%). Moderate genotypic coefficient of variation was observed in number of leaves per plant (17.94%), fresh rhizome yield per plant (14.41%), dry rhizome yield per plant (14.36%) and plant height (11.02%). The characters like leaf area (9.15%), harvest index (9.11%), number of tillers per plant (9.05%), essential oil content (7.50%) and oleoresin (7.48%) recorded lower values of genotypic coefficient of variation.

4. Discussion

The estimates of variance included phenotypic, genotypic and environmental variance, genotypic and phenotypic coefficient of variation (%). The genotypic variance varied from 0.002 for harvest index to 1246.20 for fresh rhizome yield plant^{-1} while the phenotypic variance varied from 0.005 for harvest index to 3595.27 for fresh rhizome yield plant^{-1}. The environmental variance ranged from 0.003 for harvest index to 2349.07 for fresh rhizome yield plant^{-1}. The phenotypic coefficient of variation (PCV) ranged from 7.88% for oleoresin to 43.40% for stomatal conductance (Table 2). High PCV was observed for photosynthetic rate, pollen fertility percentage, leaf area index and fresh rhizome yield plant^{-1}. The genotypic coefficient of variation (GCV) ranged from 6.24% for dry matter production to 39.06% for stomatal conductance. High GCV was observed for pollen fertility percentage, leaf area index and photosynthetic rate.

For all examined traits, PCV estimates were often greater than GCV estimates. It denotes the presence of the greatest genetic variability, which highlighted the extensive potential for selection to enhance these features. In this experiment genotypic variance was high for fresh rhizome yield plant^{-1}, plant height and number of leaves plant^{-1}. High genotypic variance for fresh rhizome yield per plant was also obtained by [8].

Similar reports were also obtained in many other studies [10, 11, 16]. On the other hand, high coefficient of variation was observed for characters like stomatal conductance, photosynthetic rate and fresh rhizome yield plant^{-1} while high heritability was observed for characters like stomatal conductance, pollen fertility percentage, leaf area, leaf area index, number of leaves plant^{-1}, plant height and oleoresin and the highest estimate of genetic advance was found in stomatal conductance, pollen fertility percentage, leaf area index, number of leaves plant^{-1} and photosynthetic rate indicating that selection for these characters in ginger could be more effective due to additive gene action. Genetic variability of crop plants is known to be fixed through ongoing selection for yield and quality attributes [7].

Table 2: Genetic parameters of fourteen characters in the selected genotypes of ginger

Sl. No.	Characters	Genotypic variance	Phenotypic variance	Environmental variance	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Coefficient of variation (%)
1	Plant height	59.08	72.85	13.77	12.23	11.02	5.32
2	Number of tillers per plant	0.63	1.84	1.21	15.46	9.05	12.53
3	Number of leaves per plant	239.79	260.20	20.41	18.69	17.94	5.24
4	Leaf area	18.36	22.65	4.29	10.16	9.15	4.42
5	Leaf area index	6.70	7.17	0.47	26.58	25.68	6.82
6	Essential oil content	0.008	0.017	0.009	10.94	7.50	7.96
7	Oleoresin	0.22	0.242	0.02	7.88	7.48	2.48
8	Dry matter production	34.48	61.64	27.16	8.34	6.24	5.54
9	Harvest index	0.002	0.005	0.003	14.40	9.11	11.15
10	Fresh rhizome yield per plant	1246.20	3595.27	2349.07	24.48	14.41	19.78
11	Pollen fertility percentage	281.95	323.31	41.36	30.74	28.71	10.99
12	Stomatal conductance	10.81	13.34	2.54	43.40	39.06	18.93
13	Photosynthetic rate	0.72	1.75	1.04	42.00	26.83	32.32

5. Conclusion

Genetic parameters were recorded mainly to comprehend the degree to which the observed variation was due to genetic factors. Genotypic and phenotypic variance was found to be highest for fresh rhizome yield per plant (1246.20 and 3595.27 respectively) followed by pollen fertility percentage (281.95 and 323.31 respectively). The phenotypic and genotypic coefficient of variation was found to be highest for stomatal conductance (43.40% and 39.06% respectively). High GCV and PCV was also observed for characters like photosynthetic rate, pollen fertility percentage and leaf area index.

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