



Study of the Genetic Diversity of Ginger

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Abstract

The experiment was carried out at the research field of Spices Research Centre, Shibganj, Bogra, Bangladesh to find out the Genetic diversity among 20 germplasms of Ginger (*Zingiber officinale* Rosc.) during Rabi 2013-14 using morphological traits. D² analysis of 20 ginger lines and analysis of variance were done. The lines were grouped into five clusters. The inter-cluster distance was larger than the intra-cluster distances. Maximum inter-cluster distance was found between cluster I and IV (48.17) followed by cluster III and IV (42.55) and me and II (30.97) and me and V (27.84). It may be concluded that the line in cluster I (15) and the line in cluster III (3, 5, and 11) grouped here is superior to all other clusters and could be used for future breeding work.

Keywords: Genetic diversity, Ginger, *Zingiber officinale* Rosc

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1. INTRODUCTION

Ginger (*Zingiber officinale* Rosc.) is one of the major spices crop in Bangladesh, has got a wide range of cultivars in terms of yield and adaptability. Zingiberaceae is a valued medicinal crop and has been used as a spice for over 2000 years [1]. It is cultivated in many tropical and subtropical countries in which, China and India are the world's leading producers [2]. The importance of ginger is gaining recently because of its low toxicity and its broad spectrum of biological and pharmacological applications including antitumor, antioxidant, anti-inflammatory, antiapoptotic, cytotoxic, anti-proliferative and anti-platelet activities [9,10,11,12]. Since ginger can be grown in sandy loamy to loam soils, so its' evaluation and selection can be essential from available germplasm for boost up national production to reduce bulk import.

In Bangladesh, ginger grows well in Rangpur, Nilphamari, Tangail, Rangamati, Bandarban, Khagrachari and Chittagong district [3]. Systematic study is therefore, needed to evaluate the existing germplasm of ginger. Crop genetic resources with a broad genetic base and high variability are vital to crop improvement program. Assessment and characterization of the state of the existing genetic diversity within the taxon is critical for planning a meaningful breeding strategy [4]. Thinking the idea in mind 20 lines was evaluated to know their performances in Bangladesh. The variability among different lines of a species is known as genetic diversity. Genetic diversity arises either due to geographical separation. D² statistic proposed by Mahalanobi's [7] is one of the potent techniques for measuring the genetic divergence both in intra and intercluster level. Genetic diversity plays an important role in plant breeding for the development of high yielding varieties. Such a study also permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations. The present study was undertaken in order to find out suitable lines on the basis of genetic diversity.

2. MATERIALS AND METHODS

This experiment was conducted at SRC, Bogra during April 2013 to February 2014 to select the promising ginger germplasms for releasing a variety. Nineteen different ginger lines (G001, G003, G004, G0010, G0011, G0012, G0020, G0021, G0022, G0023, G0024, G0025, G0026 G0026₁, G0027, G0028, G0029, G0030, G0031) and BARI Ginger-1 as check were evaluated based on their yield and other characters. Rhizomes were planted on 23 April 2013 maintaining 50 cm x 25 cm spacing in the unit plot of 3.0 m x 1.8 m size. The experiment was laid out in randomized complete block design with three replications. The size of the seed rhizome was 40-45g. In addition to 5 t/ha of cow dung, the crop was fertilized with N₁₄₀ P₅₄ K₁₁₇ S₂₀ Zn₃B₁ kg/ha. The entire quantity of cow

The genetic difference between clusters was reflected in their cluster means. Mean values for different clusters are presented in Table 4. The highest mean values for rhizome yield (t/ha), yield/plant (g), weight of primary and secondary rhizome per hill (g), dry matter (%), number of leaves/plant were observed in cluster I (Table 4). This means, lines included in this group was better for those parameters. The highest plant height was found in cluster III. Cluster IV had the lowest value for plant height. The cluster mean for disease infection (%) was highest in cluster IV and the lowest mean value was in cluster I. The lowest dry matter (%) was found in cluster IV.

Table 4. Cluster means for 9 different characters of 20 ginger lines

Characters	Clusters				
	I	II	III	IV	V
Plant height (cm)	68.5	62.1	71.8	57.8	65.4
No. of tillers/plant	31.5	20.1	28.3	16.9	24.4
No. of leaves/plant	364.8	245.6	313.1	190.7	272.7
Wt. of primary rhizome/hill (g)	46.2	36.9	45.9	30.9	40.9
Wt. of secondary rhizome/hill (g)	569.7	350.3	501.8	277.6	400.9
Rhizome yield/plant (g)	449.4	253.0	390.3	214.0	336.4
Rhizome yield (t/ha)	30.0	16.9	25.9	14.3	22.6
Dry matter (%)	29.8	23.9	28.7	23.8	26.8
Disease infection (%)	8.0	31.4	11.4	39.9	22.9

Contribution of the characters towards divergence is presented in Table 5. Results showed that, vector I obtained from CVA expressed that the important characters responsible for genetic divergence in the major axis of differentiation were disease infection (%). Plant height (cm), number of tillers/plant, no. of leaves/hill, weight of primary and second rhizome/hill (g), yield/plant (g), yield (t/ha) and dry matter (%) showed negative value in respect to vector I. In vector II, which is the second axis of differentiation, the responsible characters were plant height (cm), number of tillers/plants, number of leaves/hill and weight of primary and secondary rhizome/hill (g) played their major role on genetic divergence. The other characters of both the axis played a minor role in the genetic divergence. This means that considerable emphasis should be given on those parameters responsible for genetic divergence. Maximum contribution of disease infection (%), weight of secondary rhizome/hill (g), weight of primary rhizome/hill (g), yield/plant (g) and yield t/ha towards diversity of ginger was also found.

Table 5. Contribution of different character towards divergence in ginger

Characters	Vector I	Vector II
Plant height (cm)	-0.326	0.078
No. of tillers/plant	-0.341	0.101
No. of leaves/plant	-0.339	0.214
Wt. of primary rhizome/hill	-0.338	0.215
Wt. of secondary rhizome/hill	-0.336	0.350
Rhizome yield/plant (g)	-0.336	-0.242
Rhizome yield (t/ha)	-0.336	-0.236
Dry matter (%)	-0.307	-0.777
Disease infection (%)	0.342	-0.226

4. CONCLUSION

Considering plant architecture and other traits the different lines are clustered into 5 diverged groups. It is expected that genotypic lines belonging high to medium D^2 values tend to produce higher yield. It can be concluded that the line in cluster I (15) and the line in cluster III (3, 5, and 11) grouped here is superior to all other clusters and could be used for future breeding work.

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