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Estimation of genetic variability and identification of selection criteria based on character association and path analysis in Ginger (*Zingiber officinale* Rosc.) germplasm lines

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ABSTRACT
The experimental material comprising of 22germplasm lines collected from important ginger growing regions of Himachal Pradesh and Manipur were examined to assess genetic variability, association among component traits and their direct and indirect effects on rhizome yield to design strategy for ginger improvement. The material was evaluated in randomized complete block design with three replications during kharif 2014. Sufficient genetic variability was observed for yield and yield contributing traits. Phenotypic and genotypic coefficients of variation (PCV and GCV) were high for number of leaves per plant, weight of primary rhizome fingers and fresh rhizome yield per plant. High heritability coupled with high genetic advance was observed for number of leaves per plant, weight of primary rhizome fingers and rhizome yield per plant. Correlation studies revealed that rhizome yield per plant had positive and significant association with plant height, pseudo-stem length, leaf length, leaf breadth, number of tillers per plant, number of primary fingers per rhizome, rhizome breadth and weight of primary rhizome fingers. In view of the direct and indirect contributions of component traits, primary rhizome fingers had maximum direct effect on rhizome yield per plant so the trait can be considered a paying preposition for selection and evolving high yielding genotypes of ginger.
Key words: *Genetic, PCV, GCV, Heritability, correlation, Path analysis*

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INTRODUCTION

Ginger (*Zingiber officinale* Rosc.), is an important tropical spice crop belonging to the family Zingiberaceae which is an indispensable spice due to its aroma, flavour and medicinal properties. It is one of the most important and most widely used hot spices worldwide [1]. It has medicinal properties like stimulative, carminative, digestive and diuretic [2].

India is the largest producer and exporter of the ginger but the productivity is far below than other countries like USA, China and Indonesia [3]. Exclusive vegetative propagation in ginger limits the variability in the germplasm. The cultivated types are mainly land races, and a few high-yielding varieties released are not popular with farmers due to inadequate multiplication and distribution of seed material. In addition cultivation of outdated varieties that have become obsolete and a plethora of biotic and abiotic stresses limit the productivity in India. therefore, it is a basic need to develop high yielding varieties with better quality to increase the production and productivity of ginger in India [4].

The success of any breeding programme depends on the nature and magnitude of genetic variability present in the germplasm [5]. Availability and the knowledge of usable germplasm is a prerequisite for crop improvement. In fact, Ginger is a subterranean stem (rhizome) modified for the vegetative propagation and conventional hybridization programmes have been reported to be ineffective due to rare flowering and seed setting [6]. The major breeding achievements can be obtained from selection of the superior types out of the available germplasm and using clonal selection or non-conventional breeding approaches like tissue culture, soma clonal variations etc. Therefore, collection, conservation and evaluation of germplasm are essential for present as well as future crop improvement programmes. [7] suggested that genetic resources, particularly from clones available on farms, can be useful sources to capture and utilize diversity for conservation as well as further improvement in ginger.

Yield is a complex trait affected by a number of component traits and their association. Efficiency of indirect selection depends upon the magnitude of association between yield and target yield components [8]. Selection, therefore, be more effective if it is based on component characters rather than directly on yield [9]. Correlation coefficients, in general, show association among characters which is not sufficient to describe their relationship when the causal association among characters is needed [10]. The correlation *per se* does not give the complete picture of their interrelationships when more than two variables are involved [11]. The path analysis has been used by the breeders to identify traits that are useful selection criteria to improve crop yield [12]. Keeping this in view, present investigation was undertaken to gather information on genetic variability in 22 germplasm lines of ginger.

MATERIALS AND METHODS

The present investigation was conducted at the Instructional Farm of Krishi Vigyan Kendra, Dhaulakuan, Sirmour, Himachal Pradesh (468 m above the mean sea level with 30º4' N latitude and 71º5' E longitude) representing sub-montaneous and low hill sub-tropical conditions during *Kharif* 2014. The experimental field is characterized as clay loam soil with pH ranging from 5.8 to 6.0.

The experimental material for present study comprised of 22 genotypes of ginger including check "Himgiri". The genotypes were sown on 31st may 2014 in randomized complete block design with three replications. Each genotype was assigned a net plot size of 3.0 m × 1.35 m with row to row and plant to plant spacing of 45 × 15 cm respectively. The experimental field was brought to a fine tilth by 4-5 ploughings followed by leveling. Well decomposed farm yard manure @ 20 tonnes per hectare was added before last ploughing. For sowing, large shiny rhizomes, free from spots or marks, bud or eye injury were selected and cut into pieces of 3-5cm in the length, 15-20gm in weight and with atleast one sound bud were used. Pre sowing treatment of the rhizomes was performed after cutting rhizomes by steeping in a fungicidal suspension of Indofil M-45 (250g) and Bavistin 50 WP (100g) in 100 litre of water for 60 minutes. Fertilizers (Nitrogen, Phosphorus and Potassium) were applied at the time of sowing @ 100:50:50 kg/ha. The application of nitrogen was given as a split dose, half dose at the time of sowing while the rest quantity was applied in two splits at the time of hoeing after one month and another split a month later. The experimental field was mulched with dry leaves for keeping the field weed free. First irrigation was given after few days of sowing. Afterwards field was irrigated every 15 days interval, though irrigation was discontinued when frequent rains started during monsoon. Recommended package and protective measures were followed for proper establishment and raise a healthy crop. Four hand weedings were carried out at 3-4 weeks interval to keep the fields weed free.

The observations were recorded from five randomly selected competitive plants from each treatment in each replication and replication wise mean data was used for statistical analysis for thirteen diverse traits viz. plant height (cm), pseudo stem length (cm), leaf length (cm), leaf breadth (cm), number of leaves per plant, number of tillers per plant, rhizome length (cm), rhizome breadth (cm), number of primary rhizome fingers, inter-nodal length of primary rhizome fingers (cm), weight of primary rhizome fingers(g), weight of mother rhizome (g) and fresh rhizome yield per plant (kg).

The data collected were subjected to analysis of variance [13]. The parameters of variability, heritability in broad sense and genetic advance (GA) resulting from selection of the top 5 per cent of individuals were calculated as per the formulae of [14] and [15]. Phenotypic and genotypic coefficients of correlation were computed following [16]. The path coefficient analysis of various characters with rhizome yield was done following [17].

RESULTS AND DISCUSSION

Ginger is prone to sexual reproduction constraints, high variability and broad genetic base therefore become imperative to have sound basis for effective selection in ginger [18,19]. An insight into the magnitude of genetic variability present in a crop provides the basis for effective selection [20] and possibility to improve the yield and quality through strategic breeding programme [21]. Significant differences among all the genotypes were revealed as per the analysis of variance (ANOVA) for all the characters studied exhibiting thereby the presence of sufficient genetic variability in the genotypes (Table 1). Geographical spread accompanied by genetic differentiation into locally adapted populations caused by mutation, could be the main factor responsible for the variability observed [22]. The estimates of PCV were higher than corresponding GCV for all the characters studied (Table 2) which indicated that the apparent variation is not only due to genotypes but also due to the influence of environment. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotype alone as environmental variation is unpredictable in nature. PCV and GCV were high for number of leaves per plant, weight of primary rhizome fingers and fresh rhizome yield per plant. These high estimates indicated substantial variability ensuring ample scope for improvement of these traits through selection

[23]. Earlier workers like [24, 25, 26] have also reported high PCV and GCV for weight of primary rhizome fingers, number of leaves per plant and fresh rhizome yield per plant. Moderate estimates of PCV and GCV were observed for majority of the traits namely, leaf breadth, number of tillers per plant, inter-nodal length of primary rhizome fingers and rhizome breadth. The moderate estimates suggest that selection for the improvement of genotypes for these traits should be taken up with caution [27]. Plant height and leaf length exhibited low PCV and GCV while moderate PCV with low GCV was observed for pseudo-stem length and rhizome length signifying that selection will not be effective regardless of the significantly different mean square observed for the concerned characters.

The magnitude of heritability in broad sense indicates the reliability with which a genotype can be recognized by its phenotypic expression [28]. High heritability estimates were observed for number of leaves per plant, rhizome breadth, weight of primary rhizome fingers and fresh rhizome yield per plant. These high estimates revealed the lesser influence of environment and greater role of genetic component of variation. High heritability estimates for fresh rhizome yield per plant indicated that large proportion of phenotypic variance was attributable to the genotypic variance and the differences for the trait among the genotypes were real. The response to selection for different characters showing high heritability needs to be given due emphasis for effective selection as these characters were under genetic control. It should be noted that heritability estimates are always unique to the population under study, the growing conditions, and the experimental design used [29]. However, the high heritability does not necessarily mean high genetic gain and is insufficient alone to make improvement through simple phenotypic selection. The heritability estimates are more beneficial when used to estimate genetic advance [30] and hence, the genetic advance provides an edge over heritability as a guiding factor to breeders in various selection programmes [31]. The expected genetic advance expressed as per cent of mean was observed to be high (>30%) for number of leaves per plant, number of tillers per plant, weight of primary rhizome fingers, weight of mother rhizome fingers and rhizome yield per plant.

For estimating the actual effects of selection, heritability alone is not the sole indicator for improvement since high heritability does not mean high expected genetic advance [30]. Genetic advance may or may not be in proportion to genetic variability and heritability estimates because both high estimates of heritability and genetic variability are important to obtain higher genetic gain. Therefore, prediction on the basis of both heritability and genetic advance simultaneously could be more useful [27]. Keeping this in view, high heritability along with high genetic advance was observed for number of leaves per plant, weight of primary rhizome fingers and rhizome yield per plant (Table 2) suggesting the importance of additive gene action and hence these characters are likely to respond better to selection. However, [24] observed low heritability and genetic advance for number of leaves per plant. These variations in findings could be attributed to differences in genetic material and growing conditions.

Correlation analysis:

The effectiveness of any breeding or selection program depends upon the nature of association between yield and other component characters.Selection for yield may not be effective unless other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercise for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Therefore, after getting the knowledge on the nature and magnitude of genetic variation, it is also important to gather information on association of yield with other characters and among themselves. In general, the genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic ones (Table 3) which revealed that though there is a strong inherent association between various characters, the phenotypic expression of the correlation gets reduced under the influence of environment [32]. [25] and [33] also found genotypic correlation coefficients higher than their respective phenotypic correlation coefficients for most of the characters in ginger.

Rhizome yield per plant had significant positive correlation at both phenotypic and genotypic levels with plant height, pseudo-stem length, leaf length, leaf breadth, number of tillers per plant, number of primary fingers per rhizome, rhizome breadth and weight of primary rhizome fingers. Number of primary fingers per rhizome was observed to have the highest positive genotypic correlation with rhizome yield per plant followed by weight of primary rhizome fingers and number of tillers per plant.

Among important component traits for yield, number of tillers per plant depicted significantly positive correlation with number of primary fingers per rhizome, rhizome length, rhizome breadth and weight of primary rhizome fingers. [33] also stated that number of tillers per plant was dependent upon number of primary fingers per rhizome because of its highest positive correlation with the trait. Number of primary fingers per rhizome was found significantly in positive correlation with rhizome length and weight of primary rhizome fingers. Correlation among number of primary fingers and weight of primary fingers was very high suggesting the obvious increase of total weight of fingers with increase in number of primary fingers indicating their inter dependence. [25] have also reported similar results. On the basis of

correlation studies and their coefficients of determination, it can be concluded that the selection for number of primary rhizome fingers, weight of primary rhizome fingers and tillers per plant can be effective for isolating plants with higher yield. Plant height, pseudo-stem length, leaf length, leaf breadth, rhizome length and rhizome breadth are other important traits for selection as evident from the correlation analysis results.

Path analysis:

The end product, yield has often been described as the product of its component traits which show inter-dependence [34]. It is quite likely that the contribution of a component showing high significant association with yield may get diluted through the interaction with other components. Path analysis provide an effective means of partitioning direct and indirect causes of association while permitting a critical examination of the specific forces producing a given correlation and measuring the relative importance of each factor and thus, helps in assessing the cause-effect relationship as well as effective selection. The direct effects obtained at genotypic level were markedly different from those at phenotypic level (Table 4). These differences might be due to varying degree of influence of environment on various traits studied, which were also observed from the results of component variance analysis and correlation studies. The results also revealed contrasting effects with positive to negative direction and vice-versa among phenotypic and genotypic effects. Such a change in direction and magnitude may be attributed to environmental factors. It also indicates that the path analysis at the phenotypic level may not provide a true picture of direct and indirect causes and therefore, it would be advisable to understand the contribution of different traits at genotypic level. Weight of primary rhizome fingers had highest positive direct effect upon rhizome yield per plant at both phenotypic and genotypic level suggesting it as the most important trait regarding rhizome yield. At genotypic level highest positive direct effect of weight of primary rhizome fingers was followed by high direct effects of leaf length, weight of mother rhizome and number of tillers per plant. Similar results were observed by [35] for weight of primary rhizome fingers and for leaf length [36]. Pseudo-stem length and plant height had considerably high negative direct effects. Similar findings for plant height were observed by [33] who reported negative direct effect on rhizome yield per plant indicating that a restricted simultaneous selection for this trait may be effective. Among indirect effects, weight of primary rhizome fingers and leaf length substantially enhanced the magnitude of total correlation of all the characters having significant correlation with rhizome yield per plant. At genotypic level leaf length enhanced the magnitude of correlation towards yield for plant growth characteristics (plant height, pseudo-stem length, leaf length and leaf breadth) except tillers per plant. Similarly, Weight of primary rhizome fingers boosted the correlation coefficient of all the characters having significant correlation with yield. A critical analysis of direct and indirect effects of various traits on rhizome yield per plant also revealed that all the characters showed a negative indirect effect via plant height and pseudo-stem length. Though the plant height and pseudo-stem length showed significant positive association, its negative direct and indirect contribution indicates the inappropriateness of selecting this character for improving the rhizome yield. In conclusion, overall results suggest that weight of primary rhizome fingers as the most important trait followed by leaf length and number of tillers per plant. [35] also observed weight of primary rhizome fingers as a reliable component in breeding programme of ginger for increased potential and thus, it would be a paying preposition for evolving high yielding genotypes. The low magnitude of unexplained variation (residual effect) in the present study indicated that the traits included in the present investigation accounted for the greater part of the variation present in the dependent variable i.e. rhizome yield. Based on the results of the study, sufficient variability among the genotypes was observed while weight and number of primary rhizome fingers were identified as pivotal characters for improvement based on path analysis and correlation studies.

Table 1: Analysis of variance for different characters in ginger

Source of variation	df	Plant height (cm)	Pseudo-stem length (cm)	Leaf length (cm)	Leaf breadth (cm)	Number of leaves per plant	Number of tillers per plant	Number of Primary fingers/ rhizome	Internodal length of primary fingers	Rhizome length (cm)	Rhizome breadth (cm)	Weight of primary fingers (g)
Replication	2	39.20	3.74	2.56	0.10	483.92	2.01	0.55	0.00	8.27*	0.09	19.38
Genotypes	29	37.45*	21.19*	5.63*	0.26*	3606.36*	10.82*	1.41*	0.03*	5.43*	2.12*	645.01*
Error	58	5.26	6.30	2.31	0.06	76.21	0.87	0.28	0.00	1.27	0.15	30.93

*Significant at 5%level of significance

Table 2 Estimates of parameters of variability for different characters in ginger genotypes

Characters	GCV (%)	PCV (%)	Heritability h^2_{bs} (%)	Genetic advance % of mean
Plant height (cm)	7.43	9.08	67.10	12.54
Pseudo-stem length (cm)	7.48	11.27	44.08	10.23
Leaf length (cm)	5.57	9.78	32.45	6.54
Leaf breadth (cm)	10.36	14.28	52.57	15.47
Leaves per plant (no)	23.04	23.77	93.92	45.99
Tillers per plant (no)	17.02	19.13	79.18	31.21
Primary fingers per rhizome (no)	16.07	21.13	57.86	25.18
Inter-nodal length primary fingers (cm)	13.69	17.23	63.17	22.42
Rhizome length (cm)	9.51	13.18	52.10	14.14
Rhizome breadth (cm)	14.60	16.19	81.39	27.14
Weight of primary rhizome fingers (g)	20.42	21.91	86.87	39.21
Weight of mother rhizome (g)	17.54	20.46	73.49	30.98
Fresh rhizome yield per plant (kg)	27.89	29.91	86.97	53.59

PCV: Phenotypic Coefficient of variation; GCV: Genotypic Coefficient of Variation; h^2_{bs} (%): Heritability in broad sense; GA: Genetic Advance (%) of mean

Table 3: Phenotypic (P) and genotypic (G) correlation coefficients among different characters in ginger genotypes

Traits		Plant height	Pseudo-stem length	Leaf length	Leaf breadth	No. pf leaves/plant	No. of tillers/ plant	No. of Primary fingers/ rhizome	Inter-nodal length of primary fingers	Rhizome length	Rhizome breadth	Weight of primary rhizome fingers	Weight of mother rhizome
Rhizome yield per plant	G	0.42*	0.38*	0.31*	0.50*	0.02	0.89*	0.95*	0.15	0.42*	0.29*	0.91*	0.20
	P	0.37*	0.24*	0.25*	0.38*	0.03	0.79*	0.65*	0.09	0.23	0.25*	0.87*	0.19
Plant height	G		0.76*	0.77*	0.59*	0.31*	0.46*	0.36*	0.27*	0.01	-0.07	0.41*	0.16
	P		0.48*	0.52*	0.30*	0.23	0.38*	0.31*	0.07	0.03	-0.00	0.34*	0.14
Pseudo-stem length	G			0.77*	0.61*	0.61*	0.29*	0.57*	0.11	0.05	-0.05	0.48*	0.15
	P			0.37*	0.28*	0.38*	0.17	0.24	0.15	0.12	0.02	0.34*	0.16
Leaf length	G				0.63*	0.41*	0.31*	0.32*	0.22	0.30*	0.16	0.25*	-0.07
	P				0.30*	0.26	0.26*	0.19	0.11	0.18	0.09	0.21	0.04
Leaf breadth	G					0.27*	0.43*	0.22	0.28*	0.19	-0.02	0.34*	0.38*
	P					0.20	0.37*	0.16	0.19	-0.04	0.03	0.31*	0.35*
Leaves per plant	G						-0.04	-0.00	0.23	0.05	0.07	0.09	0.30*
	P						-0.02	-0.01	0.19	0.06	0.08	0.08	0.26*
Tillers per plant	G							0.77*	0.04	0.38*	0.36*	0.87*	-0.20
	P							0.57*	0.02	0.30*	0.37*	0.78*	-0.06
Primary fingers per rhizome	G								0.04	0.35*	0.08	0.92*	0.05
	P								-0.00	0.30*	0.11	0.58*	0.07
Inter-nodal length of primary fingers	G									0.31*	-0.07	-0.02	0.52*
	P									0.18	-0.10	-0.02	0.35*
Rhizome length	G										0.24*	0.39*	-0.19
	P										0.27*	0.22	-0.04
Rhizome breadth	G											0.35*	-0.46*
	P											0.29*	-0.25*
Weight of primary rhizome fingers	G												-0.06
	P												-0.01

*Significant at 5%level of significance

Table 4 Phenotypic and genotypic path coefficient of rhizome yield with different characters

Traits		Plant height	Pseudo-stem length	Leaf length	Leaf breadth	No. of leaves /plant	No. of Tillers /plant	No. of primary fingers/ rhizome	Inter-nodal length primary fingers	Rhizome length	Rhizome breadth	Weight of primary rhizome fingers	Weight of mother rhizome	Fresh rhizome yield per plant
Plant height	P	0.01	-0.04	0.03	0.00	-0.02	0.07	0.05	0.00	0.00	0.00	0.22	0.03	0.37*
	G	-0.47	-0.62	0.88	-0.06	0.00	0.10	0.03	-0.01	0.00	0.01	0.49	0.08	0.42*
Pseudo-stem length	P	0.01	-0.09	0.02	0.00	-0.03	0.03	0.04	0.01	0.00	0.00	0.21	0.04	0.24*
	G	-0.36	-0.81	0.88	-0.07	0.00	0.07	0.04	0.00	-0.01	0.01	0.57	0.07	0.38*
Leaf length	P	0.01	-0.03	0.06	0.00	-0.02	0.05	0.03	0.00	0.00	0.00	0.13	0.01	0.25*

	G	-0.36	-0.63	1.14	-0.07	0.00	0.07	0.02	-0.01	-0.09	-0.03	0.29	-0.04	0.31*
Leaf breadth	P	0.00	-0.02	0.02	0.02	-0.02	0.07	0.02	0.01	0.00	0.00	0.20	0.07	0.38*
	G	-0.27	-0.49	0.72	-0.11	0.00	0.10	0.02	-0.01	-0.05	0.00	0.41	0.19	0.50*
Leaves per plant	P	0.00	-0.03	0.01	0.00	-0.07	0.00	0.00	0.01	0.00	0.00	0.05	0.06	0.03*
	G	-0.15	-0.49	0.47	-0.03	0.01	-0.01	0.00	-0.01	-0.01	-0.01	0.10	0.15	0.02*
Tillers per plant	P	0.00	-0.01	0.02	0.01	0.00	0.20	0.09	0.00	0.00	0.01	0.50	-0.01	0.79*
	G	-0.21	-0.24	0.36	-0.05	0.00	0.22	0.06	0.00	-0.11	-0.06	1.03	-0.10	0.89*
Primary fingers per rhizome	P	0.00	-0.02	0.01	0.00	0.00	0.11	0.15	0.00	0.00	0.00	0.37	0.02	0.65*
	G	-0.17	-0.46	0.36	-0.02	0.00	0.17	0.07	0.00	-0.10	-0.01	1.09	0.02	0.95*
Inter-nodal length primary rhizome fingers	P	0.00	-0.01	0.01	0.00	-0.01	0.00	0.00	0.04	0.00	0.00	-0.01	0.08	0.09
	G	-0.12	-0.09	0.25	-0.03	0.00	0.01	0.00	-0.03	-0.09	0.01	-0.02	0.27	0.15
Rhizome length	P	0.00	-0.01	0.01	0.00	0.00	0.06	0.05	0.01	-0.02	0.01	0.14	-0.01	0.23
	G	-0.00	-0.03	0.34	-0.02	0.00	0.09	0.03	-0.01	-0.28	-0.04	0.46	-0.09	0.42*
Rhizome breadth	P	-0.00	-0.00	0.01	0.00	-0.01	0.07	0.02	0.00	0.00	0.04	0.19	-0.05	0.25*
	G	0.03	0.04	0.19	0.00	0.00	0.08	0.01	0.00	-0.07	-0.17	0.42	-0.23	0.29*
Weight of primary rhizome fingers	P	0.00	-0.03	0.01	0.00	-0.01	0.15	0.09	0.00	0.00	0.01	0.64	0.00	0.87*
	G	-0.19	-0.39	0.28	-0.04	0.00	0.19	0.07	0.00	-0.11	-0.06	1.19	-0.03	0.91*
Weight of mother rhizome	P	0.00	-0.01	0.00	0.01	-0.02	-0.01	0.01	0.02	0.00	-0.01	-0.01	0.21	0.19
	G	-0.07	-0.12	-0.08	-0.04	0.00	-0.04	0.00	-0.01	0.05	0.08	-0.07	0.51	0.20

*Significant at 5%level of significance Residual effect :Phenotypic = 0.13
:Genotypic = -0.08

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