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Variability, heritability and genetic advancement for yield and yield contributing characters in *Alpinia galanga* (L.) Willd

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Abstract
The experiment on genotypic variability, heritability and genetic advance for yield and yield contributing characters in fourteen *Alpinia galanga* (L.) Willd accessions were carried out at the Division of Floriculture and Medicinal crops, ICAR-IIHR, Bengaluru during the year 2019-20. Data were recorded on the parameters like plant height (cm), leaf length (cm), leaf width (cm), leaf area (cm^2), petiole length (cm), inflorescence length (cm), Flower bud size (cm), pedicel length (cm), relative height between androecium and gynoecium (cm) and yield/tiller (g). The genotypic coefficient of variation was less than the phenotypic coefficient of variation in all the characters studied. The phenotypic coefficient of variation as well as the genotypic coefficient of variation was higher for the characters like petiole length, leaf area and inflorescence length. Broad sense heritability values showed high heritability for characters like petiole length (83.35%), plant height (74.47%), leaf length (68.95%), which was on par with leaf area and inflorescence length (68.03%) and pedicel length (64.87%). The Higheest estimates of GAM were recorded for traits like petiole length (52.72%), inflorescence length (31.26%), leaf area (29. 38%) and pedicel length (23.47%).

Keywords: *Alpinia galanga*, variability, heritability and genetic advance

Introduction
Western Ghats are one of the world's richest biodiversity centre which harbours most of the plants with known and unknown medicinal significance (Krishnan *et al.,* 2011) [8]. Among various plant species, *Alpinia galanga* is one of the endemic species of Western Ghats that grows widely in tropical and subtropical regions. *Alpinia galanga* is a herbal perennial rhizomatous plant (Borthakur *et al.,* 1999) [1], belongs to the medicinally and economically significant family Zingiberaceae. It is popularly known as Greater galangal. There are several vernacular names to this plant in different languages. In Hindi, it is known as Kulanjan; Dhumarasmi, Sugandhavachi in Kannada; Mahabaracach, Sugandha Vacha, Rasna in Sanskrit; Arattha, Kol-inji, Pararatta Pararatta in Malayalam; Pedda-dhumpa in Telugu and Pera-rattai in Tamil (Verma *et al.,* 2011) [17]. Rhizomes are the economic part which are extensively used in Indian system of medicine to cure various ailments like fever, dyspepsia, rheumatic pains, kidney stones, skin diseases, bronchitis, chest pain, disease of heart, lumbago, etc. Recent studies revealed about the anticancerous, antiamoebic, antimalarial, antiallergic, anti-diabetic activities and even anti- HIV properties (Verma *et al.,* 2011) [17]. It is commonly found in Indonesia, India, China, and Arabic gulf areas, Malaysia, Egypt and Sri Lanka (Jatoi *et al*., 2006) [6]. In India it is distributed in the Himalaya and Southern region of Western Ghats (Shetty and Monisha*,* 2015) [12]. Even though distribution is seen widely in India, the population in the wild is reducing exponentially in the last few years in their natural habitat due to destructive harvesting of the rhizomes, deforestation and habitat loss. Also it requires huge planting material per hectare as seed propagation is not a commercial method of propagation in multiplying the species in the wild, which has led this species being named in the red list of medicinal plants species reported by FRLHT (Foundation for Revitalisation of Local Health Tradition- 1997) [4]. Keeping all the above aspects in view, an experiment was conducted to know the morphological variability as research work supporting the morphological characterization in this crop is very meager. In any crop, morphological characterization is an essential first step in the description and classification of plant germplasm because a stipulated breeding program in any crop mainly depends upon the magnitude of genetic variability (Smith and Smith, 1989) [14]. In the present study, fourteen accessions of *Alpinia galanga* were evaluated to know the genetic variability and also to identify elite genotypes with desirable traits for further research.

Materials and Methods
The experiment on *Alpinia galanga* (L.) Willd was carried out at the Division of Floriculture and Medicinal crops, ICAR-IIHR, Bengaluru during the year 2019-20 to find out variability, heritability and genetic advance in *Alpinia galanga* accessions. Fourteen accessions of 10 years old plants were selected for the study. Randomized block design (RBD) was adopted with three replications. Characters studied in the experiment were plant height (cm), leaf length (cm), leaf width (cm), leaf area (cm^2), petiole length (cm), inflorescence length (cm), Flower bud size (cm), pedicel length (cm), relative height between androecium and gynoecium (cm) and yield / tiller (g). Observations recorded and statistical procedure adopted during the course of investigation are described below. The phenotypic coefficient of variation and genotypic coefficient of variation was worked out as per the methods suggested by Burton and Devane (1953) [2].

$$\text{Genotypic co} - \text{efficient of variation (GCV): GCV (\%)} = \frac{\sqrt{\sigma_g^2}}{\overline{X}} \times 100$$

$$\text{Phenotypic co} - \text{efficient of variation (PCV): PCV (\%)} = \frac{\sqrt{\sigma_P^2}}{\overline{X}} \times 100$$

Where,
$\overline{X}$ = General mean
r = Number of replications
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

The PCV and GCV range are classified as follows (Subramanian and Menon, 1973) [15].
0 – 10%: Low
10 – 20%: Moderate
Above 20%: High

Heritability
Broad sense heritability was defined as the ratio of genotypic variance to the phenotypic variance and expressed in percentage (Falconer, 1981) [3].

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,
h^2 (%) = Heritability (Broad sense)
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

As suggested by Johnson *et al.* (1955) [7], heritability values are categorized as follows:
Low: Less than 30%
Moderate: 30 - 60%
High: More than 60%

Genetic advance (GA)
Genetic advance (GA) was computed using the formula given by Robinson *et al.* (1949) [10] GA = i.P.h^2

Where,
i = Selection differential (2.06) at 5 per cent selection intensity
P = Phenotypic standard deviations
h2 = Heritability at broad sense

Genetic advance as percentage over mean (GAM)
Genetic advance as percentage over mean was worked out as given by Johnson *et al.* (1955) [7]

$$\text{Genetic advance over mean (GAM)} = \frac{GA}{\overline{X}} \times 100$$

Where,
GA = Genetic advance
$\overline{X}$ = General mean

The genetic advance as per cent of mean was categorized as suggested by Johnson *et al.* (1955) [7] and the same is given below.
0-10%: Low
10-20%: Moderate
Above 20%: High

Results and Discussion
Variability
Genetic variability is considered as one of the important breeding component for the improvement of a plant species (Govindaraj *et al.*, 2015) [5]. Such information helps in locating suitable parental lines for crop improvement. Hence, to make the selection better, it is essential to study variability existing in germplasm into genetic, phenotypic and environmental variability. In the present research work, the genotypic coefficient of variation (GCV) was found to be less than the phenotypic coefficient of variation (PCV) in all the characters studied. The phenotypic coefficient of variation as well as the genotypic coefficient of variation was higher for the characters *viz.*, petiole length, leaf area and inflorescence length. The results indicated that genetic component in total variation is more and environmental influence is less in case of these traits. Thus, the selection scheme planned based on these characters will have a great selection response. Moderate GCV and PCV were observed for yield per tiller, pedicel length and leaf length, Whereas low GCV and PCV were observed for plant height, leaf width and flower bud size (Table 1). The above findings clearly indicate that the character with moderate and high magnitude of GCV and PCV suggests the existence of some variability in the population. Therefore, selection for the above traits can also be beneficial for crop improvement.
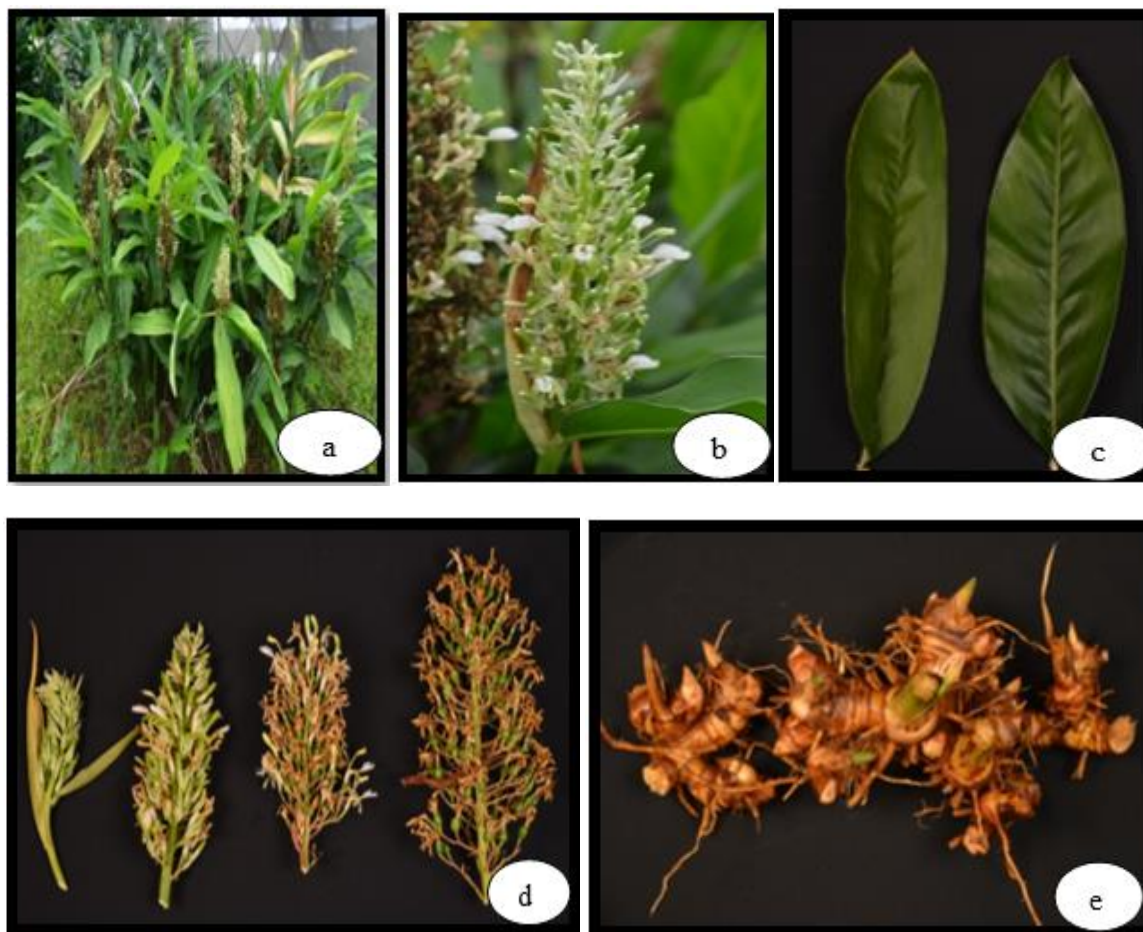
Plate 1: *Alpinia galanga* a.plant b. flower c. variation in leaves d. Different stages of development of inflorescence e. rhizomes

Table 1: Variability, heritability and genetic advance for growth and yield parameters in *Alpinia galanga* (L.) Willd accessions.

Sl. No.	Characters	Mean	GV	PV	GCV (%)	PCV (%)	h² (%)	GAM (%)
1	Plant height (cm)	187.36	260.28	349.50	8.61	9.98	74.47	15.84
2	Leaf length (cm)	39.97	16.56	24.02	10.18	12.26	68.95	17.41
3	Leaf width (cm)	10.46	0.63	1.28	7.60	10.82	49.31	10.99
4	Leaf area (cm²)	331.50	3355.65	4976.71	17.42	21.28	68.03	29.38
5	Petiole length (cm)	0.63	0.03	0.04	28.03	30.71	83.35	52.72
6	Inflorescence length (cm)	25.00	21.16	31.11	18.40	22.31	68.03	31.26
7	Flower bud size (cm)	3.08	0.03	0.07	5.56	8.35	44.24	7.61
8	Pedicel length (cm)	0.62	0.01	0.01	14.15	17.56	64.87	23.47
9	Relative height (cm) b/w androecium and gynoecium	3.505	0.13	0.25	10.55	14.37	53.97	15.97
10	Yield/tiller (g)	374.43	2390.65	4665.50	13.05	18.24	52.14	19.25

PV: Phenotypic variance,   GV: Genotypic variance,
PCV: Phenotypic coefficient of variance,   GCV: Genotypic coefficient of variance,
h² :Broad sense heritability,   GAM :Genetic advances as per cent of mean

Heritability and genetic advance
Heritability is a key to the measure, how well differences in genes account for differences in their traits. The estimation of heritability gives an idea about the amount of observed variability, which is inherent and attributed to the genetic difference (Tuppad *et al*., 2017) [16]. Even though estimation of broad sense heritability may give criteria for selection but to arrive at reliable conclusion heritability and genetic advance should be considered jointly (Jhonson *et al*., 1955) [7]. In the present study, heritability ranged from 44.24 per cent in flower bud size to 83.35 per cent in the number of pedicel length. It is found to be high for characters like petiole length (83.35%), plant height (74.47%), leaf length (68.95%), which was on par with leaf area and inflorescence length (68.03%) and pedicel length (64.87%). Similarly, high heritability estimates were also reported by Tuppad *et al*.

(2017) [16], Shruthi *et al*. (2018) [13] and Sandesh *et al*. (2018) [11]. In the present investigation, high genetic advance over mean coupled with high heritability was observed in characters like petiole length (52.72%), inflorescence length (31.26%), leaf area (29. 38%) and pedicel length (23.47%). Moderate genetic advance as per cent of mean was recorded in yield per tiller, leaf length, plant height and leaf width (Table 1). From the heritability estimates it is clear that these characters are less influenced by the environmental factors and controlled by the additive gene effect.

Conclusion
In the present study, high GCV and PCV were observed for petiole length, leaf area and inflorescence length, while high heritability coupled with high genetic advance over mean was observed for petiole length, plant height, leaf area, leaf length

and inflorescence length. Hence, the higher heritability coupled with moderate to high genetic advance values observed for these traits in the present investigation suggests that the existing variability among the accessions with respect to the traits were governed by additive genes (Panse, 1957) [9] and selection will be beneficial for the improvement of such traits.

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