

Original Research Article

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Variability, Heritability and Genetic Advance for Yield and Yield Contributing Characters in *Holostemma ada-kodien* – A Vulnerable Medicinal Plant

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ABSTRACT

The experiment was conducted during 2015-2016 at Division of Plant Genetic Resources, Indian Institute of Horticultural Research (IHR), Hessarghatta, Bengaluru. Genotypic variability, heritability and genetic advance for yield and yield contributing traits were studied on 13 *Holostemma ada-kodien* accessions. Data were recorded on plant height (m), leaf length (cm), leaf width (cm), petiole length (cm), pedicel length (cm), fruit length (cm), fruit diameter (cm), thickness of pericarp (cm), thickness of mesocarp (cm), number of fruits per plant, fruit yield (kg). Very little differences were observed between genotypic coefficient of variation and phenotypic coefficient of variation for all the characters except thickness of pericarp, thickness of mesocarp and fruit yield per plant indicating that they were less influenced to environmental factors for their phenotypic expression. Broad sense heritability values revealed high heritability for fruit length (97.75 %), petiole length (94.87 %), pedicel length (94.12 %), number of fruits per plant (92.89 %), plant height (90.61 %), leaf length (87.80 %), fruit diameter (86.82%), leaf width (85.86 %) and thickness of mesocarp (62.50 %). The highest GAM was recorded for number of fruits per plant (78.73 %), petiole length (65.47 %), pedicel length (47.27%), leaf width (39.88 %), plant height (31.36 %), leaf length (29.80 %), fruit length (25.91 %), thickness of pericarp (22.90 %).

Keywords

Holostemma ada-kodien, Variability, Heritability, Genetic advance.

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Introduction

Holostemma ada-kodien a species indigenous to India and popularly known as Jivanti or Jivani is a twiny, laticiferous perennial medicinal shrub belonging to the family Asclepiadaceae (Martin, 2002). There are several vernacular names of *H. ada-kodien* in different languages. In Sanskrit, it is known as

Jivanti; Arane beeru, Jeeva haale, Maruligana kasa in Kannada; *Holostemma* in English; Chirvel, Kanju in Hindi and Adapatian, Atapatiyan in Malayalam (Joy *et al.*, 1998). The roots are used for cough, fever, ophthalmic diseases, stomachache, dysentery, tuberculosis, arrested urination, scorpion bite,

kidney stones, goiter etc. The species is widely distributed in the tropical rain forests of the world including India, West peninsula, Srilanka and China (Sivarajan and Balachandran, 1994). In India, maximum distribution is seen in the forests of Andhra Pradesh, Tamil Nadu and Western Ghats of Karnataka and Kerala. Though distributed widely throughout Southern India, the population in wild is gradually reducing due to the destructive and ruthless collection of root tubers for ayurvedic drug preparations and fruit set is a major problem in multiplying the species in wild, which has led to the species being listed as vulnerable medicinal plant in FRLHT red list (Pushparajan and Surendran, 2014).

In India, very little research work has been done for the genetic improvement of this crop. The basic key to bring about genetic improvement to a crop is to utilize the available or created genetic variability. If the variability in the population is largely due to genetic cause with least environmental effect, the probability of isolating superior genotype is possible. The success of any crop improvement programme depends on the magnitude of genetic variability and extent to which the desirable characters are heritable. The ultimate goal of breeding programme aims to improve the characteristic of plants. As fruit yield is a polygenic trait and is associated with many agronomic, morphological and physiological traits, so direct selection for yield may be often misleading. For the selection of desirable types, the knowledge of the magnitude and direction of inter-relationship between yield and its component characters has more importance in breeding programmes. The characters showing high heritability along with high estimates of genetic advance are more effective for selection (Kalloo, 1985). Keeping the above point of view, the present investigation was taken up.

Materials and Methods

The experiment on *Holostemma ada-kodien* was carried out during 2015-16 at Division of Plant Genetic Resources, Indian Institute of Horticultural Research (IIHR), Hessarghatta, Bengaluru to find out variability, heritability and genetic advance in *Holostemma ada-kodien* accessions. Thirteen accessions collected from different places of Karnataka (9-accessions) and Kerala (4-accessions). Randomised block design (RBD) was adopted with three replications. The fertilizer applications and other cultural practices were followed as per the recommendations. Parameters studied in the experiment were plant height (m), leaf length (cm), leaf width (cm), petiole length (cm), pedicel length (cm), fruit length (cm), fruit diameter (cm), thickness of pericarp (cm), thickness of mesocarp (cm), number of fruits per plant, fruit yield (kg). Observations were recorded on an individual plant basis from three randomly selected plants per genotype in a replicate. The Phenotypic and Genotypic Coefficient of Variation was worked out as per the methods suggested by Burton and Devane (1953).

Genotypic co-efficient of variation (GCV)
(%) = $\frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$

Phenotypic co-efficient of variation (PCV)
(%) = $\frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$

Where,

\bar{X} = General mean

R = Number of replications

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The PCV and GCV are classified as follows (Subramanian and Menon, 1973).

0 - 10%: Low
10 - 20%: Moderate
Above 20%: High

Broad sense heritability was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage (Falconer, 1981).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 (%) = Heritability (Broad sense)
 σ^2_g = Genotypic variance
 σ^2_p = Phenotypic variance

As suggested by Johnson *et al.*, (1955), heritability values are categorized as follows:

Low: Less than 30 %
Moderate: 30 – 60 %
High: More than 60 %

Genetic advance (GA) was computed using the formula given by Robinson *et al.*, (1949)

$$GA = i.P.h^2$$

Where,

i = Selection differential (2.06) at 5 per cent selection intensity

P = Phenotypic standard deviations

h^2 = Heritability at broad sense

Genetic advance as percentage over mean was worked out as suggested by Johnson *et al.*, (1955).

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

Where,

GA = Genetic advance

\bar{X} = General mean

The genetic advance as per cent of mean was categorized as suggested by Johnson *et al.*, (1955) and the same is given below.

0-10%: Low
10-20%: Moderate
Above 20%: High

Results and Discussion

Variability

The amount of genetic variation present for different desirable traits was indicated by the estimation of genetic co-efficient of variation. Genetic variability in the breeding material is important for the improvement of a plant species. Hence, in order to make selection of superior plants, it is essential to study and partition the total variability existing in a germplasm into genetic, phenotypic and environmental variability.

In the present investigation, high GCV and PCV were observed for leaf width, petiole length, pedicel length, number of fruits per plant. This indicated that genetic component in total variation is more and environmental influence is less in case of these traits. Thus, selection scheme planned based on these characters will have high selection response. Moderate GCV and PCV were observed for plant height, leaf length, fruit length and thickness of pericarp. Low GCV and PCV were observed for fruit diameter, thickness of mesocarp, fruit yield per plant (Table 1). This indicated the narrow genetic base and hence variability has to be generated in these characters either through introduction or hybridising divergent genotypes to recover transgressive segregants or by mutation

breeding. The estimates of phenotypic coefficient of variation and genotypic coefficient of variation were quite closer to each other for most of the traits. This reveals that

influence of the environment for these characters is negligible and the role of the genotypic performance for the full expression of the phenotype (Jicinska, 1981).

Plate.1 Jeevanti (*Holostemma ada-kodien*) a. young plant b. flowers c. fruit d. seeds

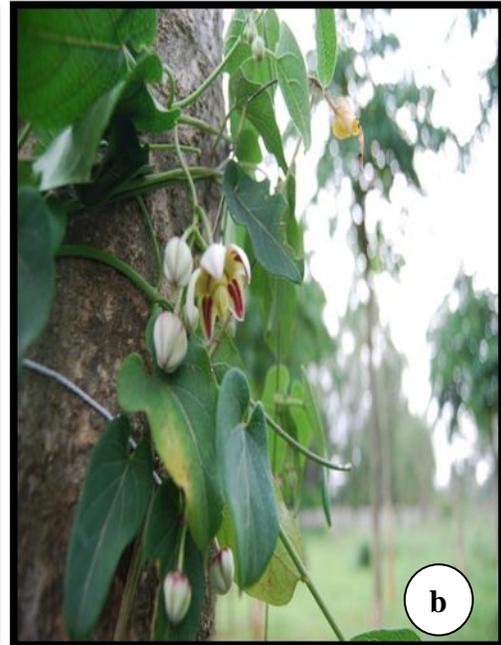


Table.1 Variability, heritability and genetic advance for growth and yield parameters in *Holostemma ada-kodien* accessions

Sl. No.	Character	Mean	GV	PV	GCV	PCV	h ² (%)	GAM (%)
1	Plant height (m)	3.010	0.232	0.256	15.991	16.799	90.61	31.36
2	Leaf length (cm)	6.290	0.943	1.074	15.436	16.473	87.80	29.80
3	Leaf width (cm)	4.069	0.723	0.842	20.892	22.547	85.86	39.88
4	Petiole length (cm)	3.282	1.147	1.209	32.627	33.498	94.87	65.47
5	Pedicle length (cm)	2.139	0.256	0.272	23.654	24.382	94.12	47.27
6	Fruit length (cm)	8.821	1.260	1.289	12.724	12.869	97.75	25.91
7	Fruit diameter (cm)	3.908	0.138	0.159	9.517	10.214	86.82	18.27
8	Thickness of pericarp (cm)	0.472	0.005	0.010	15.472	21.537	51.61	22.90
9	Thickness of mesocarp (cm)	0.717	0.005	0.008	9.862	12.475	62.50	16.06
10	Number of fruits per plant	7.385	8.575	9.231	39.651	41.140	92.89	78.73
11	Fruit yield (kg)	0.712	0.002	0.006	6.281	10.879	33.33	7.47

GV- Genotypic variance

PV- Phenotypic varianc

GCV- Genotypic co-efficient of variation

PCV- Phenotypic co-efficient of variation

h²- Broad sense heritability

GAM- Genetic advance as per cent of mean

Heritability and genetic advance

The estimation of genetic coefficient of variation indicates the amount of genetic variation present for different desirable traits. While, the heritability gives an insight into the proportion of variation which is inherent, the heritability estimates give an idea about the proportion of observed variability, which is attributed to genetic difference.

Heritability in broad sense may play greater role about information of relative value of selection in the material on the hand. Jhonson *et al.*, (1955) showed that heritability and genetic advance should be jointly considered for reliable conclusion.

Heritability estimates were high for characters like fruit length (97.75 %), petiole length (94.87 %), pedicle length (94.12 %), number of fruits per plant (92.89 %), plant height (90.61 %), leaf length (87.80 %), fruit

diameter (86.82 %) and leaf width (85.86 %). From the heritability estimates it is clear that these characters are less influenced by the environmental factors and controlled by additive gene effect.

In the present study, high genetic advance over mean coupled with high heritability was observed in characters like fruit length, petiole length, pedicle length, number of fruits per plant, plant height, leaf length, fruit diameter and leaf width. Moderate genetic advance over mean coupled with high heritability was observed in thickness of mesocarp. Yadav *et al.*, (2007) also observed high genetic advances as per cent mean for Glory lily. Hence, the higher heritability coupled with moderate to high genetic advance values observed for these traits in the present finding suggest that the existing variability among the accessions with respect to the traits is mainly due to additive type of genes (Panse, 1957).

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